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<110> University of Utah Research Foundation
              Cognetix, Inc.
              Olivera, Baldomero M.
              McIntosh, J. Michael
              Watkins, Maren
              Garrett, James E.
              Shon, Ki-Joon
              Jacobsen, Richard
              Jones, Robert M.
              Cartier, G. Edward
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	tccatgtcga ctcgctgcaa gggtaaagga aaaccatgca gtaggatttc gtataactgc 180
	tgcaccggtt cttgcagatc aggtaaatgt ggctgatcca gcgcctgatc ttcccccttc 240

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Lys Gly Lys Pro Cys Ser Arg Ile Ser Tyr Asn Cys Cys Thr Gly Ser
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       Cys Arg Ser Gly Lys Cys Gly
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             PEPTIDE
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             (1)..(25)
             Xaa at residue 7 is Pro or Hyp; Xaa at residue 13 is Tyr, 125I-Ty
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             r, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty
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                                    25
  Ser Leu Arg Ser Lys Thr Lys Leu Ser Met Ser Thr Gly Cys Met Glu
                               40
                                                   45
  Ala Gly Ser Tyr Cys Gly Ser Thr Thr Arg The Cys Cys Gly Phe Cys
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        Xaa at residue 3 is Glu or gamma-carboxy Glu; Xaa at residue 30 i
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        s Pro or Hyp; Xaa at residue 7, 21 and 29 is Tyr, 125I-Tyr, mono-
        iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty
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        Ser Leu Ser Ser Ala Thr Lys Leu Ser Met Ser Thr Arg Cys Lys Ala
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              Xaa at residue 7 is Pro or Hyp; Xaa at residue 13 is Tyr, 125I-Ty
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              r, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty
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Thr Gly Ser Cys Arg Ser Gly Lys Cys
F. 18.
                   20
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                                                                            120
      aggtcgaaga caaaactctc catgttaact ttgcgctgcg catcttacgg aaaaccttgt
                                                                            180
      ggtattgaca acgactgctg caatgcatgc gatccaggaa gaaatatatg tacgtagctg
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Ala Leu Arg Ser Lys Thr Lys Leu Ser Met Leu Thr Leu Arg Cys Ala

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       Xaa at residue 7 and 20 is Pro or Hyp; Xaa at residue 4 is Tyr, 1
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                                                                       300
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Cys Gln Leu Ile Thr Ala Glu Asp Ser Arg Gly Thr His Glu His Leu
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Ala Leu Lys Ser Thr Ser Lys Val Ser Lys Ser Thr Ser Cys Met Glu
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       Xaa at residue 6 is Glu or gamma-carboxy Glu; Xaa at residue 13,
<223>
       25 and 34 is Pro or Hyp; Xaa at residue10 is Tyr, 125I-Tyr, mono
       -iodo-Tyr, di-iodo-Tyr, -0-sulpho-Tyr or O-phospho-Ty
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Asn Xaa Asn Asn
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                                                                      240
qaatqqtaaa tgtggttgat ccagcgcctg atcttccccc ttcgtcgtgc tccatccttt
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          Conus bullatus
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          PEPTIDE
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         11, 18, 26 and 28 is Pro or Hyp; Xaa at residue 31is Trp or Bromo
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       25
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<213>
       Conus bullatus
<220>
<221>
       PEPTIDE
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pho-Ty

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         Xaa at residue 4 is Pro or Hyp; Xaa at residue 13 and 18 is Tyr,
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         У
  <400>
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                                 25
                                                      30
Ala Leu Lys Ser Thr Ser Lys Val Ser Lys Ser Thr Ser Cys Met Ala
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    50
Cys Ser Pro Phe Ser Asp Arg Cys Met Lys Lys Pro Asn Asn
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       PRT
<213>
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      Xaa at residue 13, 25 and 34 is Pro or Hyp; Xaa at residue 10 is
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       Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phos
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<400> 63

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             20
                                  25
                                                      30
Ala Leu Arg Lys Ala Thr Lys Leu Ser Val Ser Thr Arg Cys Lys Ser
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       Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O
<223>
       -sulpho-Tyr or O-phospho-Ty
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Xaa

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                                                                      321
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                                 25
                                                     30
            20
Asp Lys Asn Ser Lys Leu Thr Arg Gln Cys Ser Ala Asn Gly Gly Ser
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Ser Val Cys Val Ala Thr Ser Tyr Pro
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       Hyp; Xaa at residue 19 and 32 is Tyr, 125I-Tyr, mono-iodo-Tyr, di
       -iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty
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Ser Leu Xaa Cys Asn Lys Asp Ser Ser Val Cys Val Ala Thr Ser Xaa
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<213>---Conus-catus
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       Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O
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       -sulpho-Tyr or O-phospho-Ty
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<223> Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O
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-sulpho-Tyr or O-phospho-Ty

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	Ala Le	u Arg 35	Ser	Ala	Thr	Lys	Val 40	Ser	Lys	Ser	Thr	Ser 45	Cys	Met	Glu	
	Ala Gl 50	y Ser	Tyr	Cys	Arg	Ser 55	Thr	Thr	Arg	Thr	Cys 60	Cys	Gly	Tyr	Cys	
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              phospho-Ty
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       (1)..(26)
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       Xaa at residue 7 and 20 is Pro or Hyp; Xaa at residue 4 is Tyr, 1
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            20
                                 25
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       (1)..(25)
      Xaa at residue 7 is Pro or Hyp; Xaa at residue 13 is Tyr, 125I-Ty
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       r, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty
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                                                     30
            20
Ser Leu Arg Ser Thr Thr Lys Val Ser Lys Ala Thr Asp Cys Ile Glu
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       25 and 34 is Pro or Hyp; Xaa at residue 10, 26 and 33 is Tyr, 125
       I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty
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Ala Leu Arg Ser Asp Thr Lys Leu Ser Met Ser Thr Arg Cys Lys Gly
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       Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O
<223>
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                                                         15
                                     10
Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
                                 25
                                                     30
            20
Ala Leu Arg Ser Asp Thr Lys Leu Ser Met Ser Thr Arg Cys Lys Gly
                                                 45
        35
Lys Gly Ala Ser Cys His Arg Thr Ser Tyr Asp Cys Cys Thr Gly Ser
                        55
Cys Asn Arg Gly Lys Cys Gly
65
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<213>
      Conus consors
<220>
<221> PEPTIDE
<222>
      (1)..(25)
      Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O
<223>
       -sulpho-Tyr or O-phospho-Ty
<400> 113
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<221> misc_feature

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       114
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<211>
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<213>
       Conus consors
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ctcatcacag ctgatgactc cagaggtacg cagaagcatc gtgccctgaa gtcggacacc
                                                                      180
aaactctcca tgttaacttt gcgctgcgca tcttacggaa aaccttgtgg tatttacaac
gactgctgca atacatgcga tccagccaga aagacatgta cgtagctgat ccggcgtctg
                                                                      240
                                                                      299
atcttcccc ttctgtgctc tatccttttc tgcctgagtc_atesatacct gtgctcgag
<210>
       115
       72
<211>
<212>
       PRT
<213>
       Conus consors
<400> 115
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
                                     10
                                                         15
1
Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
            20
                                 25
                                                     30
Ala Leu Lys Ser Asp Thr Lys Leu Ser Met Leu Thr Leu Arg Cys Ala
                                                 45
                             40
        35
Ser Tyr Gly Lys Pro Cys Gly Ile Tyr Asn Asp Cys Cys Asn Thr Cys
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Asp Pro Ala Arg Lys Thr Cys Thr
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65
<210>
       116
<211> 26
<212> PRT
<213> Conus consors
<220>
<221> PEPTIDE
<222> (1)..(26)
<223> Xaa at residue 7 and 20 is Pro or Hyp; Xaa at residue 4 and 11 is
        Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-pho
       spho-Ty
<400> 116
Cys Ala Ser Xaa Gly Lys Xaa Cys Gly Ile Xaa Asn Asp Cys Cys Asn
                                     10
Thr Cys Asp Xaa Ala Arg Lys Thr Cys Thr
            20
<210> 117
<211>
       434
<212> DNA
<213> Conus consors
<220>
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<222>
                  (1)...(434)
                  n may be any nucleotide
 <223>
 <400>
                  117
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ctcatcacag ctgatgactc cagaggtacg cagaagcatc gtgccctgag gtcggacacc
                                                                                                                                                                            120
                                                                                                                                                                            180
aaactctcca tgtcgactcg ctgcaagggt acaggaaaac catgcagtag ggttgcgtat
                                                                                                                                                                            240
aactgctgca ccggttcttg cagatcaggt aaatgtggct gatccagtgc ctgatcttcc
                                                                                                                                                                            300
contrology control that control of the control of t
actcatcacc tgctcctctg gaggcttcag aggagctaca ttgaaataaa agccgcattg
                                                                                                                                                                            360
                                                                                                                                                                            420
 434
 aaaaaaaaa aaaa
 <210>
                  118
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                  71
 <212>
                  PRT
 <213>
                  Conus consors
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                  118
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
                                                                                                                                            15
                                                                                          10
 1
Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
                                                                                 25
                               20
Ala Leu Arg Ser Asp Thr Lys Leu Ser Met Ser Thr Arg Cys Lys Gly
                     35
                                                                       40
                                                                                                                        45
Thr Gly Lys Pro Cys Ser Arg Val Ala Tyr Asn Cys Cys Thr Gly Ser
          50
                                                             55
                                                                                                              60
 Cys Arg Ser Gly Lys Cys Gly
 65
 <210>
                  119
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                  25
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                  Conus consors
 <213>
 <220>
 <221>
                 PEPTIDE
                 (1)..(25)
 <222>
                 Xaa at residue 7 is Pro or Hyp; Xaa at residue 13 is Tyr, 125I-Ty
 <223>
                  r, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty
 <400> 119
 Cys Lys Gly Thr Gly Lys Xaa Cys Ser Arg Val Ala Xaa Asn Cys Cys
                                                                                                                                            15
                                                                                           10
 Thr Gly Ser Cys Arg Ser Gly Lys Cys
                               20
                                                                                 25
 <210> 120
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 <212> DNA
 <213>
                 Conus consors
 <400> 120
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    ctcatcacag ctgatgactc cagaggtacg cagaagcatc gttccctgag gtcgaccacc
                                                                          120
    aaagtctcca agtcgactag ctgcatgaaa gccgggtctt attgccgctc tactacgaga
                                                                          180
    acctgctgcg gttattgcgc ttatttcggc aaattttgta ttgactttcc cagcaactga
                                                                          240
    tcttccccct actgtgctct atccttttct gcctctgcct gagtcctcct tacctgagag
                                                                          300
   tggtcatgaa ccactcatca cctgctcccc tggaggcctc agaggagcta caatgaaata
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   aaagccgcat tgcaaaaaaa aaaaaaaaaa aaa
                                                                         393
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   <211>
          77
   <21-2>-
          PRT
   <213>
          Conus consors
   <400>
          121
   Met Lys Leu Thr Cys Met Val Ile Val Ala Val Leu Leu Leu Thr Ala
                                       10
                                                           15
  Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
                                   25
  Ser Leu Arg Ser Thr Thr Lys Val Ser Lys Ser Thr Ser Cys Met Lys
                               40
  Ala Gly Ser Tyr Cys Arg Ser Thr Thr Arg Thr Cys Cys Gly Tyr Cys
  Ala Tyr Phe Gly Lys Phe Cys Ile Asp Phe Pro Ser Asn
                      70
  <210>
         122
  <211>
         35
  <212>
         PRT
  <213>
        Conus consors
 <220>
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 <222>
        (1)..(35)
        Xaa at residue 33 is Pro or Hyp; Xaa at residue 10, 21 and 24 is
 <223>
        Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phos
        pho-Ty
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 Ser Thr Ser Cys Met Lys Ala Gly Ser Xaa Cys Arg Ser Thr Thr Arg
Thr Cys Cys Gly Xaa Cys Ala Xaa Phe Gly Lys Phe Cys Ile Asp Phe
Xaa Ser Asn
        35
<210>
      123
<211> 361
<212> DNA
<213> Conus dalli
<400> 123
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acqqcctqtc aactcatcac agctgatgac tccagaagta cgcagaagca tcgtgctctg
                                                                      120
                                                                      180
aggtcgacca tcaaacactc catgttgact aggagctgca cgcctcccgg aggaccttgt
                                                                      240
ggttattata atgactgctg cagtcatcaa tgcaatataa gcagaaataa atgcgagtag
ctgatccggc atctgatctt ccccttctgt gctcgtccta acctgagagt ggtcatgaac
                                                                      300
catcatcacc tactcctctg gaggcttcag aggagctaca tggaaataaa agccgcattg
                                                                      360
                                                                      361
С
<210>
       124
<211>
       73
<212>
       PRT
       Conus dalli
<213>
<400> 124
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala
                                                         15
                                    10
1
Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Ser Thr Gln Lys His Arg
                                                     30
            20
Ala Leu Arg Ser Thr Ile Lys His Ser Met Leu Thr Arg Ser Cys Thr
        35
Pro Pro Gly Gly Pro Cys Gly Tyr Tyr Asn Asp Cys Cys Ser His Gln
                         55
    50
Cys Asn Ile Ser Arg Asn Lys Cys Glu
65
<210>
       125
<211>
       28
<212>
       PRT
<213>
       Conus dalli
<220>
<221> PEPTIDE
      (1)..(28)
<222>
       Xaa at residue 28 is Glu or gamma-carboxy Glu; Xaa at residue 4,
<223>
       5 and 8 is Pro or Hyp; Xaa at residue 11 and 12 is Tyr, 125I-Tyr,
        mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty
<400> 125
Ser Cys Thr Xaa Xaa Gly Gly Xaa Cys Gly Xaa Xaa Asn Asp Cys Cys
                                    10
Ser His Gln Cys Asn Ile Ser Arg Asn Lys Cys Xaa
            20
                                 25
<210> 126
<211> 350
<212> DNA
<213> Conus distans
<400> 126
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                                                                       60
                                                                      120
acggcctgtc aactcactag aggaaagctg gagcgtcctg ttctgaggtc gagcgaccaa
acctccgggt caacgaagag atgcgaagat cctggtgaac cttgcggaag tgatcattcc
                                                                      180
                                                                      240
tgctgcggcg gtagttgcaa ccacaacgtc tgcgcctgaa gctggtctgg catctgacca
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<212> PRT

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300
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tctctcaata ccttctcccc tggaggcttc agaagaacta gattgaaata
<210>
      127
<211>
      66
<212>
      PRT
<213>
      Conus distans
<400> 127
Met Lys Leu Thr Cys Val Leu Ile Ile Ala Val Leu Phe Leu Thr Ala
                                  10
Cys Gln Leu Thr Arg Gly Lys Leu Glu Arg Pro Val Leu Arg Ser Ser
                              Asp Gln Thr Ser Gly Ser Thr Lys Arg Cys Glu Asp Pro Gly Glu Pro
                           40
                                              45
       35
Cys Gly Ser Asp His Ser Cys Cys Gly Gly Ser Cys Asn His Asn Val
                       55
Cys Ala
65
<210> 128
<211>
      25
<212>
      PRT
      Conus distans
<213>
<220>
<221>
      PEPTIDE
<222>
      (1)..(25)
      Xaa at residue 2 and 6 is Glu or gamma-carboxy Glu; Xaa at residu
<223>
      e 4 and 7 is Pro or Hy
     128
<400>
Cys Xaa Asp Xaa Gly Xaa Xaa Cys Gly Ser Asp His Ser Cys Cys Gly
     5
Gly Ser Cys Asn His Asn Val Cys Ala
           20
<210>
      129
<211>
      309
<212>
      DNA
<213>
      Conus ermineus
<400> 129
                                                                   60
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acagetgaeg actecagaeg taegeagaag categtgeee tgaggtegae caecaaaege
                                                                  120
                                                                  180
gccacgtcga atcgccctg caagccgaaa ggacgaaaat gttttccgca tcagaaggac
tgctgcaata aaacgtgcac cagatcaaaa tgtccctgat cttccccctt ctgtgctgta
                                                                  240
tccttttctg cctgagtcct ccttacctga gagtggtcag taaccactca tcaccatctc
                                                                  300
                                                                  309
ctctggagg
<210>
      130
<211>
      72
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<213> Conus ermineus
<400> 130
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
                                                         15
                                     10
Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Arg Thr Gln Lys His Arg
                                 25
            20
Ala Leu Arg Ser Thr Thr Lys Arg Ala Thr Ser Asn Arg Pro Cys Lys
                             40
                                                 45
        35
Pro Lys Gly Arg Lys Cys Phe Pro His Gln Lys Asp Cys Cys Asn Lys
                        55
Thr Cys Thr Arg Ser Lys Cys Pro
<210>
       131
<211>
       27
<212>
       PRT
       Conus ermineus
<213>
<220>
<221>
       PEPTIDE
<222>
       (1)..(27)
       Xaa at residue 1, 4, 11 and 27 is Pro or Hyp
<223>
<400>
       131
Xaa Xaa Lys Xaa Lys Gly Arg Lys Cys Phe Xaa His Gln Lys Asp Cys
                                     10
                                                         15
Cys Asn Lys Thr Cys Thr Arg Ser Lys Cys Xaa
            20
<210>
       132
<211>
       308
<212>
       DNA
<213>
       Conus ermineus
<400> 132
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ccaaactctc catgctgact cgggcctgct ggtcttccgg aacaccttgt ggtactgata
                                                                       120
gtttatgctg cggtggatgc aatgtatcca aaagtaaatg taactagctg attcggcgtc
                                                                       180
tgaacttccc ccttctgtgc tctatccttt tctgcccgag tcctccatac ctgagaatgg
                                                                       240
tcatgaacca ctcatcacct actcctctgg agacctcaga agagctacac tgaaataaaa
                                                                       300
                                                                       308
gcgcttgc
<210>
       133
<211>
       54
<212>
       PRT
<213> Conus ermineus
<400> 133
Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Asn Asp Arg Ala Leu
Arg Ser Thr Thr Lys Leu Ser Met Leu Thr Arg Ala Cys Trp Ser Ser
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25

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Gly Thr Pro Cys Gly Thr Asp Ser Leu Cys Cys Gly Gly Cys Asn Val
        35
Ser Lys Ser Lys Cys Asn
    50
<210>
      134
<211>
       27
<212>
       PRT
<213>
       Conus ermineus
<220>
<221>
       PEPTIDE
<222>
       (1)..(27)
      Xaa at 8 residue is Pro or Hyp; Xaa at residue 3 is Trp or Bromo
<223>
<400> 134
Ala Cys Xaa Ser Ser Gly Thr Xaa Cys Gly Thr Asp Ser Leu Cys Cys
                                    10
1
Gly Gly Cys Asn Val Ser Lys Ser Lys Cys Asn
            20
<210>
       135
<211>
       385
<212>
       DNA
       Conus geographus
<213>
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                                                                       60
                                                                      120
ctcatcacag ctgatgactc cagaggtacg cagaagcatc gtgccctggg gtcgaccacc
gaactctcct tgtcgactcg ctgcaagtca cccggatctt catgttcacc gactagttat
                                                                      180
                                                                      240
aattgctgca ggtcttgcaa tccatacgcc aaaagatgtt acggctaatc cagcgcctga
tettececet tetgtgetet atecetteet gtetgagtee teettacetg agagtggtea
                                                                      300
tgaaccactc ctcacctact tctctggagg cttcggagga gctacattga aataaaagcc
                                                                      360
                                                                      385
gcattgtaaa aaaaaaaaaa aaaaa
<210>
       136
<211>
      73
<212>
      PRT
<213> Conus geographus
<400> 136
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
                                                         15
                                     10
Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
            20
                                 25
                                                     30
Ala Leu Gly Ser Thr Thr Glu Leu Ser Leu Ser Thr Arg Cys Lys Ser
        35
Pro Gly Ser Ser Cys Ser Pro Thr Ser Tyr Asn Cys Cys Arg Ser Cys
                        55
Asn Pro Tyr Ala Lys Arg Cys Tyr Gly
65
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<213> Conus geographus

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<210>
       137
<211>
       27
<212>
       PRT
<213>
       Conus geographus
<220>
<221>
       PEPTIDE
<222>
       (1)..(27)
<223>
       Xaa at residue 4, 10 and 21 is Pro or Hyp; Xaa at residue 13, 22
       and 27 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr
        or O-phospho-Ty
<400> 137
Cys Lys Ser Xaa Gly Ser Ser Cys Ser Xaa Thr Ser Xaa Asn Cys Cys
                                                         15
                5
                                     10
Arg-Ser-Cys Asn Xaa Xaa Ala Lys Arg Cys Xaa
            20
                                 25
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       138
<211>
       396
<212>
       DNA
<213>
       Conus geographus
<400>
      138
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                                                                      120
                                                                      180
aaactcacct tgtcgactcg ctgcaaatca cccggaactc catgttcaag gggtatgcgt
gattgctgca cgccttgctt gttatacagc aacaaatgta ggcgctacta acccagcgcc
                                                                      240
tgatcttccc ccttctgtgc tctattcctt tctgcctgag tcctccttac ctgaaagtgg
                                                                      300
                                                                      360
tcatgaacca ctcatcacct acttctctgg aggcttcaga agagctacat tgaaataaaa
                                                                      396
gccgcattgc aatgacaaaa aaaaaaaaa aaaaaa
<210> 139
<211> 74
<212>
      PRT
<213> Conus geographus
<400> 139
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
                                                         15
                                     10
Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
            20
Ala Leu Arg Ser Ser Thr Lys Leu Thr Leu Ser Thr Arg Cys Lys Ser
Pro Gly Thr Pro Cys Ser Arg Gly Met Arg Asp Cys Cys Thr Pro Cys
    50
                        55
Leu Leu Tyr Ser Asn Lys Cys Arg Arg Tyr
65
<210> 140
<211> 29
<212> PRT
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<220>
      PEPTIDE
<221>
<222>
      (1)..(29)
      Xaa at residue 4, 7 and 18 is Pro or Hyp; Xaa at residue 22 and 2
<223>
       9 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O
       -phospho-Ty
<400> 140
Cys Lys Ser Xaa Gly Thr Xaa Cys Ser Arg Gly Met Arg Asp Cys Cys
Thr Xaa Cys Leu Leu Xaa Ser Asn Lys Cys Arg Arg Xaa
            20
<210>
      141
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      407
<212>
       DNA
<213> Conus geographus
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gacgtgtgtg gtgatcgtcg ccgtgctgct cctgacggcc tgtcaactca tcacagctga
                                                                     120
                                                                     180
tgactccaga ggtacgcaga agcatcgtgc cctggggtcg accaccgaac tctccttgtc
                                                                     240
gactcgctgc aagtcacccg gatcttcatg ttcaccgact agttataatt gctgcaggtc
                                                                     300
ttgcaatcca tacaccaaaa gatgttacgg ctaatccagc gcctgatctt ccctgctctg
agtcctcctt acctgagagt ggtcatgaac cactcatcac ctacttctct aggcggttcg
                                                                     360
                                                                     407
gaggagctac attgaaataa aagccgcatt gcaaaaaaaa aaaaaaa
<210> 142
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      73
<212>
      PRT
<213> Conus geographus
<400> 142
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
                                                        15
Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
Ala Leu Gly Ser Thr Thr Glu Leu Ser Leu Ser Thr Arg Cys Lys Ser
                            40
                                                45
        35
Pro Gly Ser Ser Cys Ser Pro Thr Ser Tyr Asn Cys Cys Arg Ser Cys
    50
                        55
Asn Pro Tyr Thr Lys Arg Cys Tyr Gly
65
<210>
      143
<211>
       27
<212>
       PRT
<213>
      Conus geographus
<220>
<221>
       PEPTIDE
      (1)..(27)
<222>
      Xaa at residue 4, 10 and 21 is Pro or Hyp; Xaa at residue 13, 22
<223>
       and 27 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr
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or O-phospho-Ty

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<400> 143
    Cys Lys Ser Xaa Gly Ser Ser Cys Ser Xaa Thr Ser Xaa Asn Cys Cys
                                          10
    Arg Ser Cys Asn Xaa Xaa Thr Lys Arg Cys Xaa
                 20
    <210>
           144
    <211>
           28
    <212>
           PRT
    <213>
           Conus geographus
    <220>
    <221>
           PEPTIDE
    <u>-<,2.2.2.>.</u>
           <del>-(1)...(28)</del>
   <223>
          Xaa at residue 4, 10 and 21 is Pro or Hyp; Xaa at residue 13, 22
           and 27 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr
   <400> 144
   Cys Lys Ser Xaa Gly Ser Ser Cys Ser Xaa Thr Ser Xaa Asn Cys Cys
   Arg Ser Cys Asn Xaa Xaa Thr Lys Arg Cys Xaa Gly
                                    25
   <210>
          145
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          26
  <212>
          PRT
  <213>
         Conus geographus
  <220>
  <221>
         PEPTIDE
  <222>
         (1)..(26)
         Xaa at residue 4, 10 and 21 is Pro or Hyp; Xaa at residue 13 and
  <223>
         22 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or
  <400> 145
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                                       10
 Arg Ser Cys Asn Xaa Xaa Thr Lys Arg Cys
              20
 <210>
        146
 <211> 314
 <212>
        DNA
 <213> Conus geographus
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                                                                         60
ttgctgcacg tcttgcttgt tatacagcaa caaatgtagg cgctactaac ccagcgcctg
                                                                        120
atcttccccc ttctgtgctc tattcctttc tgcctgagtc ctccttacct gaaagtggtc
                                                                        180
atgaaccact catcacctac ttctctggag gcttcagaag agctacattg aaataaaagc
                                                                       240
                                                                       300
cgcattgcaa tgac
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<210>
       147
<211>
       55
<212>
       PRT
<213>
       Conus geographus
<400>
      147
Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg Ala Leu Arg
                                    10
                                                         15
Ser Ser Thr Lys Leu Thr Leu Ser Thr Arg Cys Lys Ser Pro Gly Thr
            20
                                25
                                                     30
Pro Cys Ser Arg Gly Met Arg Asp Cys Cys Thr Ser Cys Leu Leu Tyr
                            40
        35
Ser Asn Lys Cys Arg Arg Tyr
   _5.0_ ____
<210>
       148
<211>
       29
<212>
       PRT
<213>
       Conus geographus
<220>
       PEPTIDE
<221>
       (1)..(29)
<222>
      Xaa at residue 4 and 7 is Pro or Hyp; Xaa at residue 22 and 29 is
<223>
        Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-pho
       spho-Ty
<400> 148
Cys Lys Ser Xaa Gly Thr Xaa Cys Ser Arg Gly Met Arg Asp Cys Cys
                                    10
Thr Ser Cys Leu Leu Xaa Ser Asn Lys Cys Arg Arg Xaa
                                25
            20
<210>
       149
<211>
       29
<212>
       PRT
<213> Conus geographus
<220>
<221> PEPTIDE
<222> (1)..(29)
<223> Xaa at residue 4 and 7 is Pro or Hyp; Xaa at residue 22 and 29 is
        Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-pho
       spho-Ty
<400> 149
Cys Lys Ser Xaa Gly Thr Xaa Cys Ser Arg Gly Met Arg Asp Cys Cys
                                    10
Thr Ser Cys Leu Ser Xaa Ser Asn Lys Cys Arg Arg Xaa
                                25
            20
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            20
Ala Leu Arg Ser Thr Thr Asn Leu Ser Met Leu Thr Arg Lys Cys Trp
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       Trp; Xaa at residue 8 and 27 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-
       iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty
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aggtcgacca ccaaactctc catatcgact cgctgccttc ctcccggatc atattgtaag
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gcattg	С						367
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Cys Gl	n Leu Ile	Thr Ala	a Asp Asp	Ser_Arg-Gly 25	-Thi Gin Lys 30	His Arg	
Ala Le	u Arg Ser 35	Thr Th	r Lys Leu 40	Ser Ile Ser	Thr Arg Cys	s Leu Pro	
Pro Gl 50	y Ser Tyr	Cys Lys	s Ala Thr 55	Thr Glu Val	Cys Cys Ser 60	Ser Cys	
Leu Gl	n Phe Ala	Gln Ile 70	e Cys Ser	Gly			
<210> <211> <212> <213>		terculat	tus				
<222>	nd 4 is	esidue : Pro or l	Hyp; Xaa a	_	is Tyr, 125	Kaa at residue SI-Tyr, mono-io	
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Cys Le	u Xaa Xaa	5			Thr Xaa Val	- -	
Cys Le 1 Ser Se <210> <211> <212>	u Xaa Xaa r Cys Leu	5 Gln Phe	e Ala Gln	10 . Ile Cys Ser	Thr Xaa Val	- -	
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            20
Ala Leu Arg Ser Thr Thr Asn Leu Ser Met Ser Thr Arg Cys Lys Ser
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Pro Gly Ser Ser Cys Ser Val Ser Met Arg Asn Cys Cys Thr Ser Cys
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Asn Ser Arg Thr Lys Lys Cys Thr Arg Arg Gly
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       Xaa at residue 3 is Pro or Hyp
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                                                                      180
                                                                      240
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attcggcgtc taaacttcct ccttctgcct gagtcctcca tacctgagag tggtcatgaa
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                                 25
            20
Ala Leu Arg Ser Thr Thr Lys Leu Ser Met Leu Thr Arg Thr Cys Trp
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                                                 45
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Asn Val Ser Arg Ser Lys Cys Asn
65
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       27
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       PRT
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       Xaa at residue 4 is Pro or Hyp; Xaa at residue 3 is Trp or Bromo
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Ser Gly Cys Asn Val Ser Arg Ser Lys Cys Asn
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aggtcgacca ccaatctctc catgctgact cggaagtgct ggccttccgg aagctattgt
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cgtgcgaata gtaaatgctg cagtggatgc gatcggaaca gaagtaaatg taactagctg
                                                                       240
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Ala Leu Arg Ser Thr Thr Asn Leu Ser Met Leu Thr Arg Lys Cys Trp
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120

180

240

300

360

Pro Ser Gly Ser Tyr Cys Arg Ala Asn Ser Lys Cys Cys Ser Gly Cys

Asp Arg Asn Arg Ser Lys Cys Asn

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<210>

<211>

164

27

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         <220>
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         <222>
                (1)..(27)
                Xaa at residue4 is Pro or Hyp; Xaa at residue 3 is Trp or Bromo
         <223>
                Trp; Xaa at residue 8 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Ty
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₩
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Ala Leu Arg Ser Thr Thr Lys Leu Ser Arg Ser Leu Phe Glu Cys Ala

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                         55
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       37
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<222>
       (1)..(37)
       Xaa at residue 4, 20 and 26 is Glu-or-gamma-carboxy Glu; Xaa at r
<223>
       esidue 7 and 34 is Pro or Hyp; Xaa at residue 22 and 35
       125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-T
       У
<400>
       167
Ser Leu Phe Xaa Cys Ala Xaa Ser Gly Gly Arg Cys Gly Phe Leu Lys
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Ser Cys Cys Xaa Gly Xaa Cys Asp Gly Xaa Ser Thr Ser Cys Val Ser
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            20
Gly Xaa Xaa Ser Ile
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<211>
       365
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teceegtage cettagaeta caeggetece agteaacett gtggttattt tectaggtge
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                                                                       240
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cgccttctgt gctgtatcct tttctgcctg agtcctccat acccgtgagt ggtcatgaac
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cactcaacac ctactcctct ggaggcttca gaggaactat attaaaataa agccgcattg
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caatg
       169
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<213> Conus leopardus
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                                     10
Cys Gln Leu Thr Thr Ala Asp Ile Ser Arg Gly Thr Trp Lys His Arg
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                                 25
Gly Val Gly Ser Thr Thr Gly Leu Ser Pro Trp Pro Leu Asp Cys Thr
        35
                             40
                                                 45
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Ala Pro Ser Gln Pro Cys Gly Tyr Phe Pro Arg Cys Cys Gly His Cys

55

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Asp Val Arg Arg Val Cys Thr Ser Gly
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       170
<211>
       30
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       PRT
<213>
       Conus leopardus
<220>
<221>
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<222>
       (1)..(30)
<223>
       Xaa at residue 2, 8, 11 and 16 is Pro or Hyp; Xaa at residue 1 is_
        Trp or Bromo Trp; Xaa at residue 14-is-Tyr, 1251-Tyr, mono-iodo-
       Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty
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Xaa Xaa Leu Asp Cys Thr Ala Xaa Ser Gln Xaa Cys Gly Xaa Phe Xaa
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       171
<211>
       381
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       DNA
<213>
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tccaggtcgc cctctaggtg catgtctccc ggtggaattt gtggtgattt tggtgactgc
                                                                       180
                                                                       240
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cgccttctgt gctctatcct tttctgcctg agtcctccat acccctgagt ggtcatggac
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cactcaacac ctactcctct ggaggcttca gaggaactac attaaaataa agccgcattg
                                                                       360
                                                                       381
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       172
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       Conus leopardus
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Cys Gln Leu Thr Thr Ala Asp Ile Ser Arg Gly Thr Arg Lys His Arg
            20
                                 25
                                                     30
Ala Leu Arg Ser Thr Thr Lys Leu Ser Arg Ser Pro Ser Arg Cys Met
        35
                                                 45
Ser Pro Gly Gly Ile Cys Gly Asp Phe Gly Asp Cys Cys Glu Ile Cys
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Asn Val Tyr Gly Ile Cys Val Ser Asp Leu Pro Gly Ile
65
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                                         75
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   <213>
          Conus leopardus
   <220>
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          PEPTIDE
   <222>
          (1)..(31)
         Xaa at residue 16 is Glu or gamma-carboxy Glu; Xaa at residue 4 a
   <223>
          nd 29 is Pro or Hyp; Xaa at residue 21 is Tyr, 125I-Tyr, mono-iod
         o-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty
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   Cys Met Ser Xaa Gly Gly Ile Cys Gly Asp Phe Gly Asp Cys Cys Xaa
  Ile Cys Asn Val Xaa Gly Ile Cys Val Ser Asp Leu Xaa Gly Ile
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  <211>
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         DNA
  <213>
         Conus leopardus
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                                                                     120
  tccaggtggc ccaggtactg cgcgcctccc ggtggagctt gtgggttttt tgatcactgc
                                                                     180
 tgcggatatt gcgaaacgtt ttacaatacg tgtagatgag ttggctgatc cggcgcttga
                                                                     240
 tettteegee ttetgttget etatetttt etgeetgagt eeteceatae eeegttgagt
                                                                     300
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                                                                     360
 404
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        PRT
 <213> Conus leopardus
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Cys Gln Leu Thr Thr Ala Asp Asp Ser Arg Gly Thr Arg Lys His Arg
                                25
Ala Leu Arg Ser Thr Thr Lys Leu Ser Arg Trp Pro Arg Tyr Cys Ala
Pro Pro Gly Gly Ala Cys Gly Phe Phe Asp His Cys Cys Gly Tyr Cys
Glu Thr Phe Tyr Asn Thr Cys Arg
65
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<210> 176
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      27
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<213> Conus leopardus
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<400> 179

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<222>
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<223>
       nd 5 is Pro or Hyp; Xaa at residue 1, 18 and 23 is Tyr, 125I-Tyr,
        mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty
<400> 176
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1
Gly Xaa Cys Xaa Thr Phe Xaa Asn Thr Cys Arg
            20
                                25
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<211>--292--
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                                                                      120
tccatqtcqa ctcqctqcaa qtctcccqqa tcaccatqta qtqtqacatc qtataactqc
                                                                      180
tgcacttttt gctcttcata cactaagaaa tgtcgggcct ctttatgaac cactcatcac
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ctactcctct ggaggcctca gaagagctac actgaaataa aagccgcatt gg
                                                                      292
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<211>
       75
<212>
       PRT
<213> Conus lynceus
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                                25
                                                     30
            20
Ala Leu Arg Ser Thr Thr Asn Leu Ser Met Ser Thr Arg Cys Lys Ser
        35
Pro Gly Ser Pro Cys Ser Val Thr Ser Tyr Asn Cys Cys Thr Phe Cys
                        55
Ser Ser Tyr Thr Lys Lys Cys Arg Ala Ser Leu
                    70
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65
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       30
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<213>
       Conus lynceus
<220>
       PEPTIDE
<221>
<222>
       (1)..(30)
<223>
       Xaa at residue 4 and 7 is Pro or Hyp; Xaa at residue 13 and 22 is
        Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-pho
       spho-Ty
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        gctctatcct ttttctgcct gagtcctcca tacctgagaa tggtcatgaa ccactcatca
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                                                                15
       Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
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       Ala Leu Arg Ser Thr Thr Lys Leu Ser Met Tyr Thr Arg Cys Ala Gly
                                                       45
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      Arg Thr His Leu Cys His Ser Arg Thr Gly
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      <211> 28
      <212>
             PRT
      <213> Conus lynceus
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            PEPTIDE
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            (1)..(28)
            Xaa at residue 4 and 9 is Pro or Hyp; Xaa at residue 16 is Tyr, 1
      <223>
            25I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty
     <400> 182
     Cys Ala Gly Xaa Gly Ala Ile Cys Xaa Asn Arg Val Cys Cys Gly Xaa
                                          10
                                                              15
     Cys Ser Lys Arg Thr His Leu Cys His Ser Arg Thr
                                     25
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                 DNA
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         cacgctgatg actccagagg tacgcagaag actgctgccc gaggtcgacc accaaaactc
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         tccatgctga ctcgggcctg ctggtcttcc ggaacacctt gtggtactga tagtttatgc
                                                                                 180
         tgcggtggat gcaatgtatc caaaagtaaa tgtaactagc tgattcggcg tctgaacttc
                                                                                 240
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                                                                                .0.0,
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25
30
        Ala Arg Gly Arg Pro Pro Lys Leu Ser Met Leu Thr Arg Ala Cys Trp
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       <213> Conus lynceus
       <220>
       <221> PEPTIDE
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                                   25
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  Ala Leu Arg Ser Thr Thr Asn Leu Ser Met Leu Thr Arg Lys Cys Trp
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  Asp Gln Asn Arg Asn Lys Cys Tyr
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        Trp; Xaa at residue 8 and 27 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-
        iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty
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Arg Gly Cys Asp Gln Asn Arg Asn Lys Cys Xaa
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                                          25
                                                               30
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        <213>
               Conus magus
        <220>
        <221>
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        <222>
               (1)..(25)
1-1
              Xaa at residue 7 is Pro or Hyp; Xaa at residue 13 is Tyr, 125I-Ty
        <223>
               r, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty
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       Thr Gly Ser Cys Arg Ser Gly Lys Cys
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                                                                              120
      aagtcggaca ccaaactctc catgttaact ttgcgctgcg catcttacgg aaaaccttgt
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      ggtatttaca acgactgctg caatacatgc gatccagcca gaaagacatg tacgtagctg
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<213> Conus magus

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                                 25
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Ala Leu Lys Ser Asp Thr Lys Leu Ser Met Leu Thr Leu Arg Cys Ala
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       PEPTIDE
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       Xaa at residue 7 and 20 is Pro or Hyp; Xaa at residue 4 and 11 is
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        Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-pho
       spho-Ty
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agcatcgtgc cctgaggtcg gacaccaaac tctccatgtc aactcgctgc aagggtaaag
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ttggctgatc cgcc
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<210>
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       71
<212>
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<213> Conus magus
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Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
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Ala Leu Arg Ser Asp Thr Lys Leu Ser Met Ser Thr Arg Cys Lys Gly
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     Cys Asn Arg Gly Lys Phe Gly
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    <213>
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    <222>
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 gccgtctgat attccctttc tgtgcttcat cctcttttgc ctgagtcatc catacctgtg
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 <213> Conus miles
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Thr Cys Asn Lys Leu Ile Gly Val Cys Leu
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<212>
       PRT
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      PEPTIDE
<222>
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Ala Leu Arg Ser Asp Thr Lys Leu Ser Ile Ser Thr Arg Cys Lys Ser
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<222>
      Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O
<223>
       -sulpho-Tyr or O-phospho-Ty
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          Thr Gly Ser Cys Arg Ser Gly Lys Cys
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                258
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                                                                              120
        aggtcggaca ccaacctctc catgtcgact cgctgcaagg gtaaaggatc ttcatgtagt
                                                                              180
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                                                                              240
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                                                                              258
        <210> 205
        <211>
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               PRT
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               Conus monachus
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                                        25
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       Ala Leu Arg Ser Asp Thr Asn Leu Ser Met Ser Thr Arg Cys Lys Gly
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             Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O
      <223>
             -sulpho-Tyr or O-phospho-Ty
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      Thr Gly Ser Cys Asn Arg Gly Lys Cys
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     <211>
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       Conus obscurus
<213>
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Gly Thr Thr Gly Val Cys Cys Gly Phe Cys Ser Asp Phe Gly Tyr Lys
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       Xaa at residue 2, 3 and 33 is Pro or Hyp; Xaa at residue 27 and 3
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       2 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O
       -phospho-Ty
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                                               Conus obscurus
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                                             Conus monachus
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                                            PEPTIDE
                         <222>
                                            (1)..(28)
                                           Xaa at residue 3 is Pro or Hyp
                         <223>
  <400> 212
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                       Gly Thr Cys Ser Ser Ile Leu Lys Ser Cys Val Ser
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                      <211>
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                                         Conus pulicarius
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                                                                                                                                                                                                                180
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Arg Ala Leu Arg Ser Thr Asp Lys Asn Ser Lys Leu Thr Arg Gln Cys
        35
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<221>
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       Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 4 is Pro or H
<223>
       yp; Xaa at residue 19 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Ty
       r, O-sulpho-Tyr or O-phospho-Ty
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                                                                       180
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tgctgcggtc gagcgtgcat catcacaata tgtccctgat cttccccctt ctgtgctgta
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                                                     30
Ala Leu Arg Ser Thr Thr Lys Gly Ala Thr Ser Asn Arg Pro Cys Lys
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Thr Pro Gly Arg Lys Cys Phe Pro His Gln Lys Asp Cys Cys Gly Arg
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<222>
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<223>
       Xaa at residue 1, 5, 11 and 27 is Pro or Hyp
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                                                                      180
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                                                                      240
gcagaagatt atgactgctg ccttagatgc aaagttggag gtacatgtgg ctgatccagt
gcctgatctt ccccttctg tgctctatcc ttttctgcct gagtcctcct tacctaagag
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                                     10
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                                 25
            20
Ala Leu Arg Ser Thr Thr Lys Leu Phe Thr Ser Lys Ser Cys Lys Leu
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Pro Gly Ala Tyr Cys Asn Ala Glu Asp Tyr Asp Cys Cys Leu Arg Cys
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Lys Val Gly Gly Thr Cys Gly
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<221>
      PEPTIDE
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<223>
      Xaa at residue 12 is Glu or gamma-carboxy Glu; Xaa at residue 5 i
       s Pro or Hyp; Xaa at residue 8 and 14 is Tyr, 125I-Tyr, mono-iodo
       -Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty
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Cys Leu Arg Cys Lys Val Gly Gly Thr Cys
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       Conus purpurascens
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                                                                      180
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<211> 72
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                                    10
1
Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Arg Thr Gln Lys His Arg
                                                    30
            20
Ala Leu Arg Ser Thr Thr Lys Arg Ala Thr Ser Asn Arg Pro Cys Lys
                            40
        35
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Lys Thr Gly Arg Lys Cys Phe Pro His Gln Lys Asp Cys Cys Gly Arg
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Ala Cys Ile Ile Thr Ile Cys Pro
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      (1)..(27)
<223>
       Xaa at residue 1, 11 and 27 is Pro or Hyp
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                Conus radiatus
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                                                                             120
        atcacagctg atgactccag aggtatgcag aaacatcatg ccctggggtc gatcagcagt
                                                                             180
        ctctttaagt cgacccgtca_tggctgeaaa-cccctcaaac gtcgttgttt caatgataaa
                                                                             240
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 ctgaataaaa gccgcattgc aaaaaaaa
328
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        <211>
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        <213>
               Conus radiatus
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              226
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                                            10
                                                                15
Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Met Gln Lys His His
                                       25
                                                           30
       Ala Leu Gly Ser Ile Ser Ser Leu Phe Lys Ser Thr Arg His Gly Cys
                                   40
                                                       45
Lys Pro Leu Lys Arg Cys Phe Asn Asp Lys Glu Cys Cys Ser Lys
                               55
                                                   60
       Phe Cys Asn Ser Val Arg Lys Gln Cys Gly
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      <211> 28
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      <213> Conus radiatus
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      <221> PEPTIDE
      <222> (1)..(28)
      <223>
             Xaa at residue 15 is Glu or gamma-carboxy Glu; Xaa at residue 5 i
      <400> 227
      His Gly Cys Lys Xaa Leu Lys Arg Arg Cys Phe Asn Asp Lys Xaa Cys
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      Cys Ser Lys Phe Cys Asn Ser Val Arg Lys Gln Cys
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            DNA
     <213> Conus radiatus
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ctctttaagt cgacccgtcg tggctgcaaa cccctcaaac gtcgttgttt caatgataaa
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1
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                                 25
            20
Ala Leu Gly Ser Ile Ser Ser Leu Phe Lys Ser Thr Arg Arg Gly Cys
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Lys Pro Leu Lys Arg Arg Cys Phe Asn Asp Lys Glu Cys Cys Ser Lys
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Phe Cys Asn Ser Val Arg Asn Gln Cys Gly
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       PRT
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<220>
<221>
       PEPTIDE
<222> (1)..(28)
<223> Xaa at residue 15 is Glu or gamma-carboxy Glu; Xaa at residue 5 i
       s Pro or Hy
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Cys Ser Lys Phe Cys Asn Ser Val Arg Asn Gln Cys
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<211> 435
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<213> Conus radiatus
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cggcctgtca actcatcaca gctgatgact ccagaggtat gcagaagcat catgccctga
                                                                      180
ggtcgatcac caaactctcc ctgtcgactc gctgcaaacc tcccggatca ccatgtagag
                                                                      240
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                                                                      300
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ccccttctgt gctctatcct tttcctgccc gagtcctcca tacctgagag tagtcatgaa
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                Conus radiatus
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                                         25
                                                              30
        Ala Leu Arg Ser Ile Thr Lys Leu Ser Leu Ser Thr Arg Cys Lys Pro
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Pro Gly Ser Pro Cys Arg Val Ser Ser Tyr Asn Cys Cys Ser Ser Cys
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        Lys Ser Tyr Asn Lys Lys Cys Gly
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               Conus radiatus
U
        <220>
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               PEPTIDE
        <222>
               (1)..(27)
11
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              Xaa at residue 3, 4 and 7 is Pro or Hyp; Xaa at residue 13 and 22
               is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-
              phospho-Ty
       Cys Lys Xaa Xaa Gly Ser Xaa Cys Arg Val Ser Ser Xaa Asn Cys Cys
                                            10
       Ser Ser Cys Lys Ser Xaa Asn Lys Lys Cys Gly
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       <213>
             Conus rattus
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      ttcgatacag ctgcgagcta cgacaaaggt aagcagaaac ctcctactct gaggccagct
                                                                            120
      gacaaacaca tcaggttgac caagcgttgc aatgctcgca atgatggttg cagtcaacat
                                                                            180
      tctcaatgct gcagtggatc ttgcaataag actgcaggcg tatgtctgta aagctggtct
                                                                            240
      gccgtctgat attccctttc tgtgctttat cctcttttgc ctgagtcatc catacctgtg
                                                                            300
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Pro Thr Leu Arg Pro Ala Asp Lys His Ile Arg Leu Thr Lys Arg Cys 35 40 45	
Asn Ala Arg Asn Asp Gly Cys Ser Gln His Ser Gln Cys Cys Ser Gly 50 55 60	
Ser Cys Asn Lys Thr Ala Gly Val Cys Leu 65 70	
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gacaaacact tcaggttgat caagcgttgc aatgctcgca atagtggttg cagtcaacat	180
cctcaatgct gcagtggatc ttgcaataag actgcaggcg tatgtctgta aagctggtct	240
gccgtctgat attccctttc tgtgctttat cctcttttgc ctgagtcatc catacctgtg	300
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aaagccacat tgcaacgaaa aaaaaaaaa aaaaa	395
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Cys Gln Leu Asp Ala Ala Ala Ser Tyr Asp Lys Gly Lys Gln Lys Pro

Pro Thr Leu Arg Pro Ala Asp Lys His Phe Arg Leu Ile Lys Arg Cys 35 40 45

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Asn Ala Arg Asn Ser Gly Cys Ser Gln His Pro Gln Cys Cys Ser Gly 50 55 60
Ser Cys Asn Lys Thr Ala Gly Val Cys Leu 65 70
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<220>
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<222> (1)(27) <223> Xaa at residue 12 is Pro or Hyp
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gacaaacact tcaggttgat caagcgttgc aatgctcgca atagtggttg cagtcaacat 180
cctcaatgct gcagtggatc ttgcaataag actttgggcg tatgtctgta aagctggtct 240
gccgtctgat attccctttc tgtgctttat cctcttttgc ctgagtcatc catacctgtg 300
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Pro Thr Leu Arg Pro Ala Asp Lys His Phe Arg Leu Ile Lys Arg Cys 35 40 45
Asn Ala Arg Asn Ser Gly Cys Ser Gln His Pro Gln Cys Cys Ser Gly

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Ser Cys Asn Lys Thr Leu Gly Val Cys Leu
65
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       PRT
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       Conus rattus
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<222>
       (1)..(27)
<223>
       Xaa at residue 12 is Pro or Hyp
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Gly Ser Cys Asn Lys Thr Leu Gly Val Cys Leu
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       DNA
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                                                                      180
aggettatgt atgactgetg cageggttet tgeagegget acaeaggtag atgtggetga
                                                                      240
                                                                      300
tocagogoot gatottocco ottotgtgot ctatootttt otgootgggt cotoottaco
                                                                      360
tgagagtggt catgaaccac tcatcaccta ctcctctgga ggcctcagag gagttacaat
                                                                      379
gaaataaaag ccgcattgc
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      73
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Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
            20
                                 25
                                                     30
Ala Leu Arg Ser Lys Thr Lys Leu Ser Met Ser Thr Arg Cys Lys Ser
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Lys Gly Ala Lys Cys Ser Arg Leu Met Tyr Asp Cys Cys Ser Gly Ser
                        55
Cys Ser Gly Tyr Thr Gly Arg Cys Gly
<210> 245
<211> 27
<212> PRT
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                Xaa at residue 13 and 23 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo
         <223>
                -Tyr, O-sulpho-Tyr or O-phospho-Ty
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         Cys Lys Ser Lys Gly Ala Lys Cys Ser Arg Leu Met Xaa Asp Cys Cys
         Ser Gly Ser Cys Ser Gly Xaa Thr Gly Arg Cys
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                246
        <211>
                35
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               PRT
        <213>
               Conus stercusmuscarum
 <220>
        <221>
 L.
               PEPTIDE
        <222>
               (1)..(35)
Xaa at residue 33 is Pro or Hyp; Xaa at residue 10, 21, 24 and 32
        <223>
                 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O
               -phospho-Ty
        <400>
               246
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10
2
                                                                15
Ile Cys Cys Gly Xaa Cys Ala Xaa Phe Gly Lys Lys Cys Ile Asp Xaa
                                        25
30
       Xaa Ser Asn
               35
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       <213> Conus stercusmuscarum
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      acgacctgtc aactcatcac agctgatgac tccagaggta cgcaggagca tcgtgccctg
                                                                            120
      aggtcgaaga ccaaactctc catgttaact ttgcgctgcg catcttacgg aaaaccttgt
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                                                                            380
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      <211>
             72
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             PRT
      <213>
            Conus stercusmuscarum
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                                          10
                                                              15
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Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Glu His Arg
                                                         30
    Ala Leu Arg Ser Lys Thr Lys Leu Ser Met Leu Thr Leu Arg Cys Ala
                                40
    Ser Tyr Gly Lys Pro Cys Gly Ile Asp Asn Asp Cys Cys Asn Ala Cys
                                                 60
   Asp Pro Ala Arg Asn Ile Cys Thr
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          PRT
   <213>
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   <220>
   <221>
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   <222>
          (1)..(26)
         Xaa at residue 7 and 20 is Pro or Hyp; Xaa at residue4 is Tyr, 1
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          25I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty
  <400>
         249
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                                       10
  Ala Cys Asp Xaa Ala Arg Asn Ile Cys Thr
              20
                                   25
  <210>
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  <211>
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  <213>
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                                                                       120
 aaactctcca tgttaacttt gcgctgcgta tcttacggaa aaccttgtgg tattgacaac
                                                                       180
 gactgctgca atgcatgcga tccagccaga aatatatgta cgtagctgat ccggcgtctg
                                                                       240
 atcttccccc ttctgtgctc tatccttttc tgcctgggtc ctccttacct gagagtggtc
                                                                       300
 atgaaccact catcacctac tcctctggag gcctcagagg agttacaatg aaataaaagc
                                                                       360
 cgcattgcaa aaaaaaaaa aaaaaaaa
                                                                       388
 <210> 251
<211>
       72
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<213> Conus stercusmuscarum
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                                     10
                                                         15
Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Glu His Arg
                                 25
                                                     30
Ala Leu Arg Ser Lys Thr Lys Leu Ser Met Leu Thr Leu Arg Cys Val
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40
                                                      45
     Ser Tyr Gly Lys Pro Cys Gly Ile Asp Asn Asp Cys Cys Asn Ala Cys
     Asp Pro Ala Arg Asn Ile Cys Thr
     65
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            252
    <211>
            26
    <212>
           PRT
    <213>
           Conus stercusmuscarum
    <220>
    <221>
           PEPTIDE
    <222>
           (1)..(26)
    <223> Yaa-at-residue / and 20 is Pro or Hyp; Xaa at residue 4 is Tyr, 1
           25I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty
   <400> 252
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                                        10
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   Ala Cys Asp Xaa Ala Arg Asn Ile Cys Thr
               20
                                    25
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   <211>
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          DNA
   <213>
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  acggcctgtc aactcatcac agctgatgac tccagaggta cgcagaagca tcgttccctg
                                                                         60
  aggtcgacca ccaaagtctc caaggcgact gactgcattg aagccggaaa ttattgcgga
                                                                        120
  cctactgtta tgaaaatctg ctgcggcttt tgcagtccat acagcaaaat atgtatgaac
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                                                                        240
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                                                                        264
        254
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        78
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        254
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                                     10
                                                          15
Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
Ser Leu Arg Ser Thr Thr Lys Val Ser Lys Ala Thr Asp Cys Ile Glu
Ala Gly Asn Tyr Cys Gly Pro Thr Val Met Lys Ile Cys Cys Gly Phe
Cys Ser Pro Tyr Ser Lys Ile Cys Met Asn Tyr Pro Lys Asn
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       Conus striatus
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<221>
       PEPTIDE
<222>
       (1)..(36)
<223>
      Xaa at residue 6 is Glu or gamma-carboxy Glu; Xaa at residue 13,
       25 and 34 is Pro or Hyp; Xaa at residue 10, 26 and 33 is Tyr, 125
       I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty
      255
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Ala Thr Asp Cys Ile Xaa Ala Gly Asn Xaa Cys Gly Xaa Thr Val Met
                5
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Lvs_Ile_Cys-Gys-Gly Pne Cys Ser Xaa Xaa Ser Lys Ile Cys Met Asn
                                 25
Xaa Xaa Lys Asn
        35
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       256
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       233
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       DNA
<213>
       Conus striatus
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tgctctatcc ttttctgcct gggtcctcct tacctgagag tggtcatgaa ccactcatca
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                                                                      233
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<210>
       257
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       30
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<213> Conus striatus
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Asp Cys Cys Ser Gly Ser Cys Gly Arg Arg Gly Lys Cys Gly
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                                 25
            20
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       258
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       26
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       PRT
<213>
      Conus striatus
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<221> PEPTIDE
<222>
      (1)..(26)
      Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O
<223>
       -sulpho-Tyr or O-phospho-Ty
<400> 258
Cys Lys Leu Lys Gly Gln Ser Cys Arg Arg Thr Met Xaa Asp Cys Cys
                                     10
Ser Gly Ser Cys Gly Arg Arg Gly Lys Cys
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259
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       310
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       DNA
       Conus striatus
<213>
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                                                                      120
                                                                      180
aggtcggaca ccaaactctc catgtcgact cgctgcaagg ctgcaggaaa atcatgcagt
aggattgcgt ataactgctg caccggttct tgcagatcag gtaaatgcgg ctgatccagc
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                                                                      300
                                                                      310
gtcatgaacc
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       71
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       PRT
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       Conus striatus
       260
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                5
                                     10
1
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                                                     30
                                 25
            20
Ala Leu Arg Ser Asp Thr Lys Leu Ser Met Ser Thr Arg Cys Lys Ala
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                             40
                                                 45
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                                             60
    50
                        55
Cys Arg Ser Gly Lys Cys Gly
65
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       25
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<222>
      (1)..(25)
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       -sulpho-Tyr or O-phospho-Ty
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                                     10
Thr Gly Ser Cys Arg Ser Gly Lys Cys
            20
<210>
       262
<211>
       256
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       DNA
<213> Conus striatus
<400> 262
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aggtcggaca ccaaactctc catgttaact ttgcgctgcg aatcttacgg aaaaccttgt	180
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Ala Leu Arg Ser Asp Thr Lys Leu Ser Met Leu Thr Leu Arg Cys Glu 35 40 45	
Ser Tyr Gly Lys Pro Cys Gly Ile Tyr Asn Asp Cys Cys Asn Ala Cys 50 55 60	
Asp Pro Ala Lys Lys Thr Cys Thr 65 70	
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aggactgcgt atgactgctg caccggttct tgcaacagag gtagatgtgg ctgatccagc
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Ser Leu Arg Ser Thr Thr Lys Val Ser Met Ser Thr Arg Cys Lys Gly
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Cys Asn Arg Gly Arg Cys Gly
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20 25 30	
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Arg Pro Ser Gly Ser Asn Cys Gly Asn Ile Ser Ile Cys Cys G. 50 55 60	
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aggtcgacta ccaaagtctc caagtcgact agctgcatga aagccgggtc ttatt	tccctg 120
gctactacga gaatctgctg cggttattgc gcttatttcg gcaaaatatg tattg	tgcgtc 180
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          s Pro or Hyp; Xaa at residue 1 and 11 is Tyr, 125I-Tyr, mono-iodo
          -Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty
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Ala Leu Gly Arg Thr Thr Lys Leu Thr Leu Ser Thr Arg Cys Lys Ser
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Ala Leu Gly Ser Thr Thr Lys Leu Thr Leu Ser Thr Arg Cys Leu Ser
Pro Gly Ser Ser Cys Ser Pro Thr Ser Tyr Asn Cys Cys Arg Ser Cys
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                                             60
Asn Pro Tyr Ser Arg Lys Cys Arg Gly
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       (1)..(27)
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  aggaaggcca ccaaactccc cgtgtcgact cgctgcatta ctttaggaac acgatgtaag
                                                                         180 .
  gttccgagtc aatgctgcag atcttcttgc aagaacggtc gttgtgctcc atcccctgaa
                                                                         240
  gaatggtaaa tgtggctgat ccagcgcctg atcttccccc ttctgactgt ctccgacctt
                                                                         300
  ttctgcctga gtcctcctta cctgagaggt gtcatgaacc actcatcacc tactccctg
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 Ala Leu Arg Lys Ala Thr Lys Leu Pro Val Ser Thr Arg Cys Ile Thr
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<223>
       due 11, 26 and 28 is Pro or Hyp; Xaa at residue 31 is Trp or Brom
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Cys Gln Leu Ile Thr Ala Glu Asp Ser Arg Gly Thr His Glu His Leu 20 25 25 25 26 Ala Leu Lys Ser Thr Ser Lys Val Ser Lys Ser Thr Ser Cys Met Glu 45 Ala Arg Ser Tyr Cys Gly Pro Ala Thr Thr Lys Ile Cys Cys Asp Phe 50 Cys Ser Pro Phe Ser Asp Arg Cys Met Asn Asn Pro Asn Asn 65 70 Cys Ser Pro Phe Ser Asp Arg Cys Met Asn Asn Pro Asn Asn 65 Color Ser Ser Pro Phe Ser Asp Arg Cys Met Asn Asn Pro Asn Asn 65 Cys Ser Pro Phe Ser Asp Arg Cys Met Asn Asn Pro Asn Asn 65 Cys Ser Pro Phe Ser Asp Arg Cys Met Asn Asn Pro Asn Asn 65 Cys Ser Pro Phe Ser Asp Arg Cys Met Asn Asn Pro Asn Asn 65 Cys Ser Pro Phe Ser Asp Arg Cys Met Asn Asn 65 Cys Ser Pro Phe Ser Asp Arg Cys Met Asn Asn 65 Cys Ser Pro Phe Ser Asp Arg Cys Met Asn Asn 65 Cys Ser Pro Phe Ser Asp Arg Cys Met Asn 65 Cys Met Asn 65 Cys Met Asn 65 Cys Cys Asp Phe Cys Ser Xaa Phe Ser Asp Arg Cys Met Asn 75 Asn Xaa Asn Asn 75 Asn Xaa Asn Asn 76 Cys Met Asn 76 Cys Met Asn 77 Asn Xaa Asn Asn 76 Cys Met Asn 77 Cys Met Asn 78 Cys Met Asn 79 Cys Met Asn 79 Cys Met Asn 70 Cys	1 Cys Val Ala Ile Val Ala Val Leu Leu Leu Thr Ala	
Ala Leu Lys Ser Thr Ser Lys Val Ser Lys Ser Thr Ser Cys Met Glu 35 40 45 Ala Arg Ser Tyr Cys Gly Pro Ala Thr Thr Lys Ile Cys Cys Asp Phe 50 Cys Ser Pro Phe Ser Asp Arg Cys Met Asn Asn Pro Asn Asn 65 70 Cys Ser Pro Phe Ser Asp Arg Cys Met Asn Asn Pro Asn Asn 65 C210> 296 C211> 36 C212> PRT C213> Conus viola C220> C221> PEPTIDE C222> (1)(36) C223> Xaa at residue6 is Glu or gamma-carboxy Glu; Xaa at residue 13,	Cys Gln Leu Ile Thr Ala Glu Asp Ser Arg Gly Thr His Glu His Leu	
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Lys Ile Cys Cys Asp Phe Cys Ser Xaa Phe Ser Asp Arg Cys Met Asn 20 Asn Xaa Asn Asn 35	<400> 296	
Asn Xaa Asn Asn 35	15	
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Ala Leu Arg Lys Thr Thr Lys Leu Ser Leu Ser Thr Arg Cys Lys Gly
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       У
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Lys Xaa Ser Cys Gly Asn Gly Lys Cys
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   ggttattata atgactgctg cagtcatcaa tgcaatataa acagaaataa atgtgagtag
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   ctgatccggc atctgatctg tgctcgccct aacctgagag tggtcatgaa ccactcatca
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  Ala Leu Arg Ser Thr Thr Lys His Phe Met Leu Thr Trp Tyr Cys Thr
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        no-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty
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	Gly Phe Cys Asp Met Ala Asn Asn Arg Cys Leu 20 25	
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	gacaaaaact cccagttgac cagggaatgc accctccag gtggagcttg tggtttacct 18	20
	acacactgct gcgggttttg cgatatggca aacaacagat gtctgtaaaag getat	
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       cctgttacaa ctgagacttt ctccagaggt aaggagaagc gtcgtgctct gaggtcaact
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70

Cys Asp Asn Val Ser His Thr Cys Tyr Gly Glu Thr Pro Ser Leu His

60

Ala Leu Arg Ser Asp Thr Lys Leu Pro Ile Ser Thr Arg Cys Lys Gly

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Asn Pro Asn Asn
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Pro Ser Asn
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      Conus circumcisus
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Cys Lys Gly Lys Gly Ala Ser Cys Arg Lys Thr Met Tyr Asn Cys Cys
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Ser Gly Ser Cys Ser Asn Gly Arg Cys
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         Pro Ser Asn
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       Pro Ser Asn
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      Ser His Gln Cys Asn Ile Ser Arg Asn Lys Cys Glu
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       Xaa is Hyp
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Cys Glu Asp Xaa Gly Glu Xaa Cys Gly Ser Asp His Ser Cys Cys Gly
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Pro-Cys Lys Pro Lys Gly Arg Lys Cys Phe Pro His Gln Lys Asp Cys
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Cys Asn Lys Thr Cys Thr Arg Ser Lys Cys Pro
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       Conus ermineus
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Ala Cys Trp Ser Ser Gly Thr Pro Cys Gly Thr Asp Ser Leu Cys Cys
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Gly Gly Cys Asn Val Ser Lys Ser Lys Cys Asn
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Cys Lys Ser Pro Gly Ser Ser Cys Ser Pro Thr Ser Tyr Asn Cys Cys
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Arg Ser Cys Asn Pro Tyr Ala Lys Arg Cys Tyr
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Cys Lys Ser Pro Gly Thr Pro Cys Ser Arg Gly Met Arg Asp Cys Cys
Thr Pro Cys Leu Leu Tyr Ser Asn Lys Cys Arg Arg Tyr
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                          Cys Lys Pro Pro Arg Arg Lys Cys Leu Lys Ile Lys Asp Lys Cys
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                          Asn Phe Cys Asn Thr His Leu Asn Met Cys
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                       Cys Ser Lys Arg Thr His Leu Cys His Ser Arg Thr
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                     Lys Cys Trp Pro Ser Gly Ser Tyr Cys Arg Ala Asn Ser Lys Cys Cys
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                     Ser Gly Cys Asp Arg Asn Arg Asn Lys Cys Tyr
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Harm then then the things
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Lys Cys Trp Pro Ser Gly Ser Tyr Cys Arg Ala Asn Ser Lys Cys
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Ser Gly Cys Asp Arg Asn Arg Ser Lys Cys Asn
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Gly Pro Tyr Ser Ile
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Arg Cys Cys Gly His Cys Asp Val Arg Arg Val Cys Thr Ser
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       Conus leopardus
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Cys Met Ser Pro Gly Gly Ile Cys Gly Asp Phe Gly Asp Cys Cys Glu
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       Cys Ala Ser Tyr Gly Lys Pro Cys Gly Ile Tyr Asn Asp Cys Cys Asn
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       Thr Cys Asp Pro Ala Arg Lys Thr Cys Thr
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      Gly Thr Cys Asn Lys Leu Ile Gly Val Cys Leu
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     Thr Gly Ser Cys Arg Ser Gly Lys Cys
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Ser Pro Pro Cys Met Lys Gly Gly Ser Ser Cys Arg Gly Thr Thr Gly
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Val Cys Cys Gly Phe Cys Ser Asp Phe Gly Tyr Lys Cys Arg Asp Tyr
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Pro Gln Asn
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Cys Leu Pro Asp Gly Thr Ser Cys Leu Phe Ser Arg Ile Arg Cys Cys
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Gly Thr Cys Ser Ser Ile Leu Lys Ser Cys Val Ser
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Cys Gly Arq Ala Cys Ile Ile Thr Ile Cys Pro
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        Pro Cys Lys Lys Thr Gly Arg Lys Cys Phe Pro His Gln Lys Asp Cys
        Cys Gly Arg Ala Cys Ile Ile Thr Ile Cys Pro
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              Conus pulicarius
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              385
       Gln Cys Ser Pro Asn Gly Gly Ser Cys Ser Arg His Phe His Cys Cys
                                            10
       Ser Leu Tyr Cys Asn Lys Asn Thr Gly Val Cys Ile Ala Thr
T.
噩
                                        25
                                                             30
fine from flow days
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      Glu Cys Thr Pro Pro Asp Gly Ala Cys Gly Leu Pro Thr His Cys Cys
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      Gly Phe Cys Asp Met Ala Asn Asn Arg Cys Leu
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     Gly Phe Cys Asp Met Ala Asn Asn Arg Cys Leu
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<400> 383

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   Cys Ser Lys Phe Cys Asn Ser Val Arg Asn Gln Cys
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  Gly Ser Cys Asn Lys Thr Ala Gly Val Cys Leu
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 Gly Ser Cys Asn Lys Thr Leu Gly Val Cys Leu
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Gly Phe Cys Asp Asn Val Ser His Thr Cys Tyr Gly Glu Thr Pro Ser
Leu His
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Cys Lys Ala Ala Gly Lys Ser Cys Ser Arg Ile Ala Tyr Asn Cys Cys
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Thr Gly Ser Cys Arg Ser Gly Lys Cys
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Ala Cys Asp Pro Ala Lys Lys Thr Cys Thr
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Cys Lys Ser Lys Gly Ala Lys Cys Ser Arg Leu Met Tyr Asp Cys Cys
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Ser Gly Ser Cys Ser Gly Tyr Thr Gly Arg Cys
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Pro Ser Asn
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Thr Gly Ser Cys Asn Arg Gly Arg Cys
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Ser Thr Ser Cys Met Lys Ala Gly Ser Tyr Cys Val Ala Thr Thr Arg
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Ile Cys Cys Gly Tyr Cys Ala Tyr Phe Gly Lys Ile Cys Ile Asp Tyr
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Pro Lys Asn
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Tyr Cys Thr Pro His Gly Gly His Cys Gly Tyr His Asn Asp Cys Cys
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Ser His Gln Cys Asn Ile Asn Arg Asn Lys Cys Glu
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Cys Ile Thr Leu Gly Thr Arg Cys Lys Val Pro Ser Gln Cys Cys Arg
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Ser Ser Cys Lys Asn Gly Arg Cys Ala Pro Ser Pro Glu Glu Trp
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Cys Lys Ser Arg Gly Ser Ser Cys Arg Arg Thr Ser Tyr Asp Cys Cys
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 Lys Ile Cys Cys Asp Phe Cys Ser Pro Phe Ser Asp Arg Cys Met Asn
 Asn Pro Asn Asn
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Lys Tyr Ser Cys Gly Asn Gly Lys Cys
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Ser His Gln Cys Asn Ile Asn Arg Asn Lys Cys Glu

<210> 412 <211> 27 <212> PRT <213> Conus textile

<400> 412 .

Cys Thr Pro Tyr Gly Gly His Cys Gly Tyr Asn His Asp Cys Cys Ser His Gln Cys Asn Ile Asn Arg Asn Lys Cys Glu

<210> 413 <211> 26 <212> PRT <213> Conus tulipa <220> <221> PEPTIDE <222> (1)..(26) <223>

Xaa is Hyp

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Trp Ser Cys Ser Pro Tyr Arg Lys Lys Cys